

File Name: SY-12

Created: 14:29 01-01-22
Data: Original

Measuring Mode: Abs.
Scan Speed: Fast
Slit Width: 1.0
Sampling Interval: 0.2

FIG.1

Result = (Area * Factor) / Divisor Factor = 0.000

Region	Start	End	Divisor	Area	Result
--------	-------	-----	---------	------	--------

C A M A S H C Evaluation Software

ARIBRO PHARMACEUTICALS LTD G/14 Kirti Nagar INDUSTRIAL AREA NEW DELHI
PHONE: 6467226, 515-0437, FAX: 91-11-5465784, E-mail: arbro@vsnl.com

H C/HPTLC-Integration (CATS3.18 S/N: 0207A004 / SCANNER 11 V3.14 S/N: 990602)

ESTIMATION OF L-LYSINE BY HPTLC

Libr. Table Calibration table. Created : ARIBRO PHARMA LTD
 File name : AMINO 3/JUN/ 0 14:49:45
 User name while measuring : ARIBRO PHARMA LTD
 File name : AMINO 3/JUN/ 0 14:54:52
 User while integrating : ARIBRO PHARMA LTD
 File name : AMINO 3/JUN/ 0 15:19:25

Track 1. Analysis a:
 Peak start mm h max mm h [%] end mm h area
 61.1 0.4 72.6 64.1 100.00 73.2 0.1 3136.2 100.00
 Total height = 64.1 total area = 3136.2

Track 2. Standard level 1:
 Peak start mm h max mm h [%] end mm h area
 62.9 2.8 71.0 63.5 100.00 73.3 0.6 3133.9 100.00
 Total height = 63.5 total area = 3133.9

FIG.2(a)

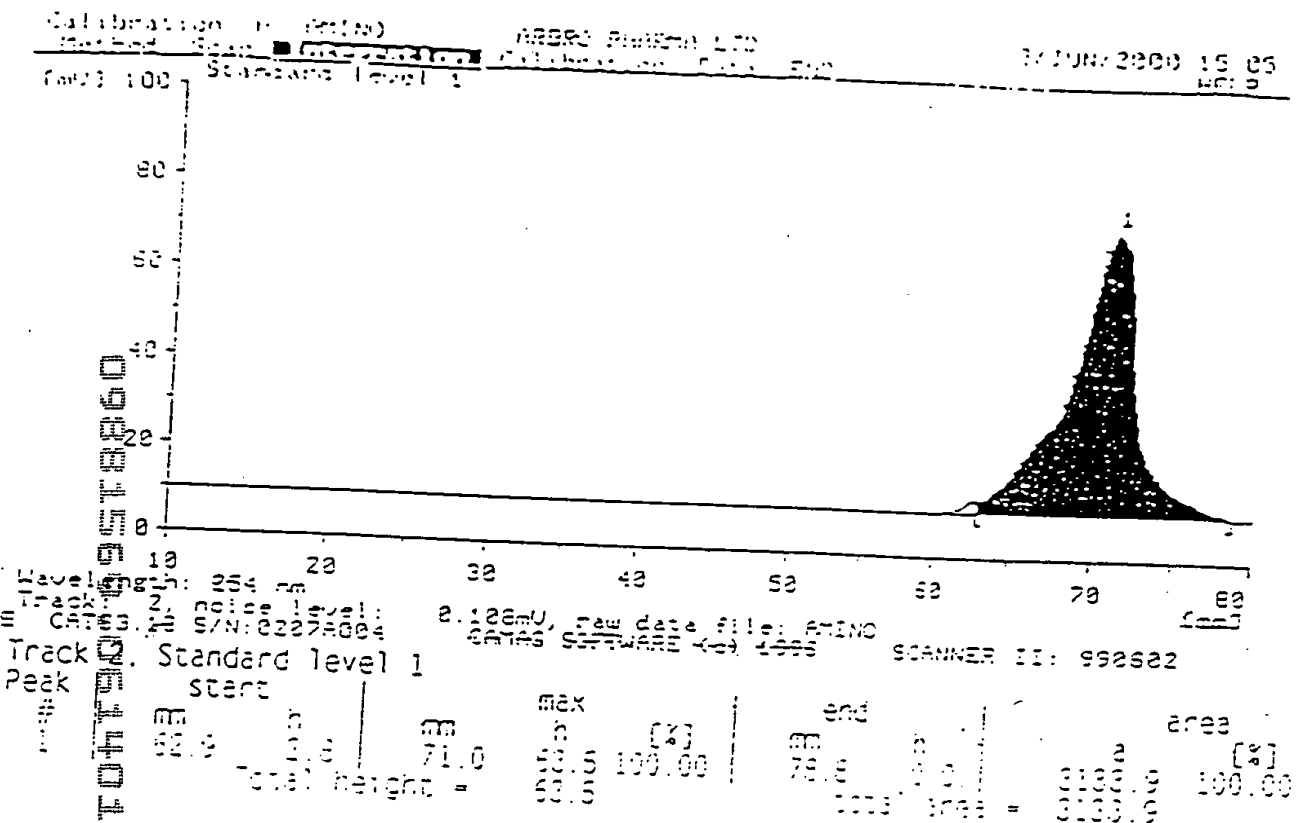


FIG.2(b)

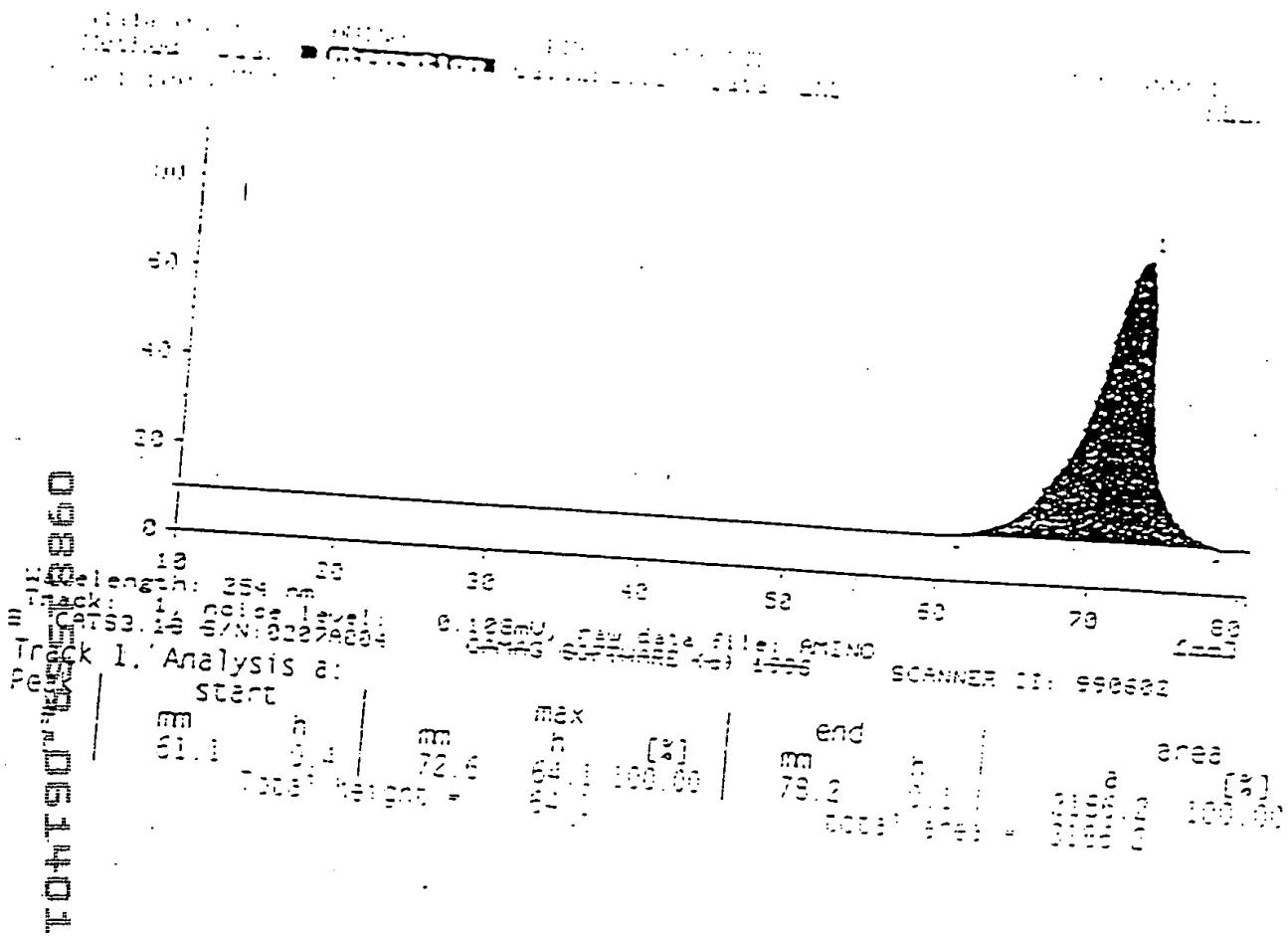


FIG.2(c)

Calibration: 11 07190 GENERO PHARMA LTD
 Method: Scan Integration Calibration Data: END
 Date: 06/06/2000 15:32
 Standard Level: 1

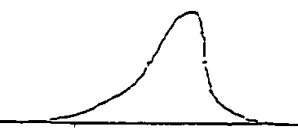
50
100



Calibration: 11 07190 GENERO PHARMA LTD
 Method: Scan Integration Calibration Data: END
 Date: 06/06/2000 15:32
 Standard Level: 1

09881569.061401

100
80
60
40
20
0



20 30 40 50 60 70 80 [min]
 S/N: 82278224 CAMAC SOFTWARE (C) 1996 SCANNER 11: 992622

FIG.2(d)

SUBMITTER : PUSHPA KHANNA

SAMPLE NAME : GOURDIN

DATE :

	ASP	LEU				TYR		SER	HIS
		VAL	SER	GLN	GLN	VAL	GLY	GLN	ARG
SEQUENCE :	GLY	ILE	GLU	GLU	THR	THR		THR	GLN
CYCLE #:	1	2	3	4	5	6	7	8	9

			ARG				GLY		
	LYS	TYR	HIS	HIS		ARG	ASP	ARG	ARG
		ILE	ALA	GLU	ASN	MET	ASN	THR	HIS
SEQUENCE :	ARG	LEU	LYS	TYR	ASP	ILE	LEU	ASP	ALA
CYCLE #:	10	11	12	13	14	15	16	17	18

	SER							PRO	
	GLU		SER		GLU		THR	ARG	HIS
	LEU	ARG	PRO	ILE	LEU	PHE	SER	ALA	ARG
SEQUENCE :	LYS	GLU	ALA	ASP	ILE	TYR	ASN	HIS	GLY
CYCLE #:	19	20	21	22	23	24	25	26	27

	GLY			VAL		PRO		
	VAL			LEU	ASN	ILE	ALA	
	ALA	GLY	ARG	ILE	SER	THR	VAL	ASN
SEQUENCE :	ALA	GLY	ARG	ILE	SER	THR	VAL	ASN
CYCLE #:	28	29	30	31	32	33	34	35

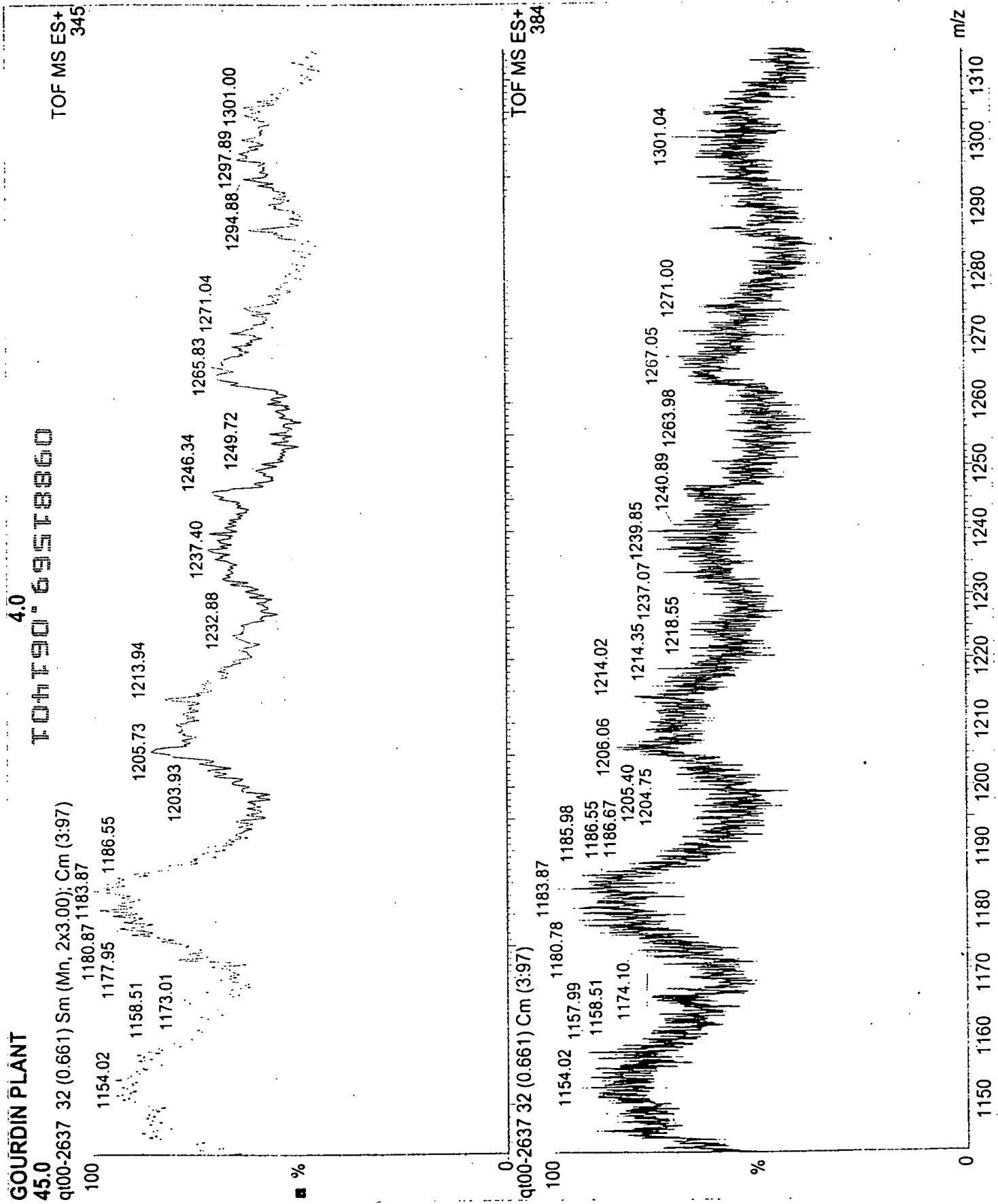
YIELD (pmol) : ILE(2) 98.11 YIELD(pmol): GLU(3) 56.13

CARRYOVER : ILE(6) 22.6% REP YIELD: ILE(2,23) 92.3%

SEQSTD YIELD :NL(6) 2.30 SEQSTD CARRYOVER : NL(6) 23.0%

SEQSTD REP YIELD : NL(6,11) 97.0%

COMMENTS : Mixtures with interchangeable amino acids at positions 12, 13, 15-19, 25-27 and 31-34. Appears to be a mixture of sequences.



TOF MS ES+ 501

GOURDIN PLANT

45.0

q100-2637 32 (0.661) Sm (Mn, 2x3.00); Cm (3:97)

943.00

100

%

713.00

816.00

831.88

855.91

941.92

943.98

1008.83

1056.90

1060.86

1183.87

1205.73

1237.40

1297.89

711.93

706.03

601.90

678.95

TOF MS ES+ 555

q100-2637 32 (0.661) Cm (3:97)

943.00

100

%

712.97

817.89

828.01

831.88

855.91

941.92

943.98

1008.83

1009.16

1128.03

1183.87

TOF MS ES+ 555

m/z

FIG. 4(b)

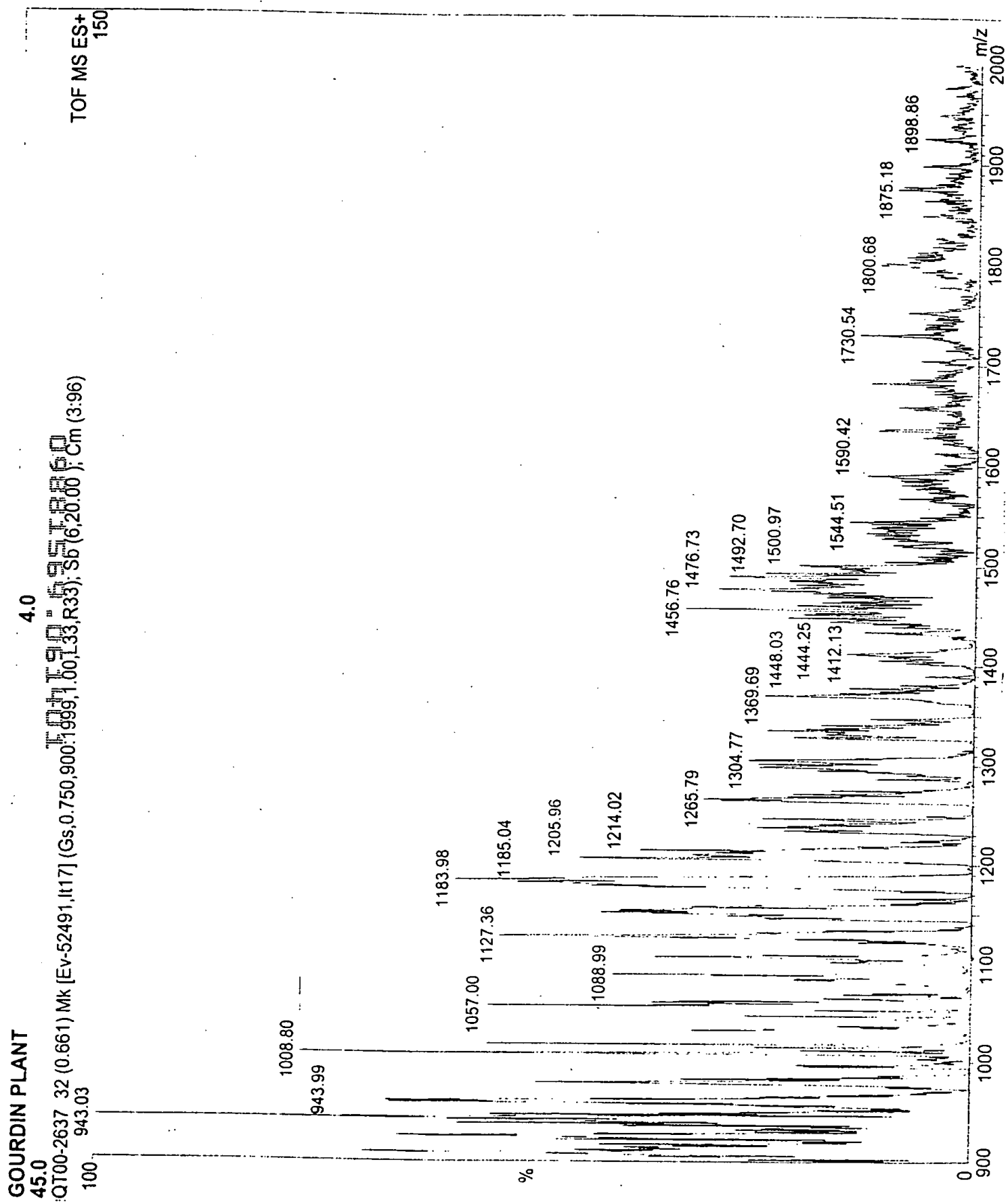


FIG. 4(c)

4.0

09881569-061401

QT00-2637 32 (0.661) M1 [Ev-52491,It17] (Gs,0.750,900:1999,1.00,L33,R33); Sb (6,20.00); Cm (3:96)

100

TOF MS ES+
1.17e3

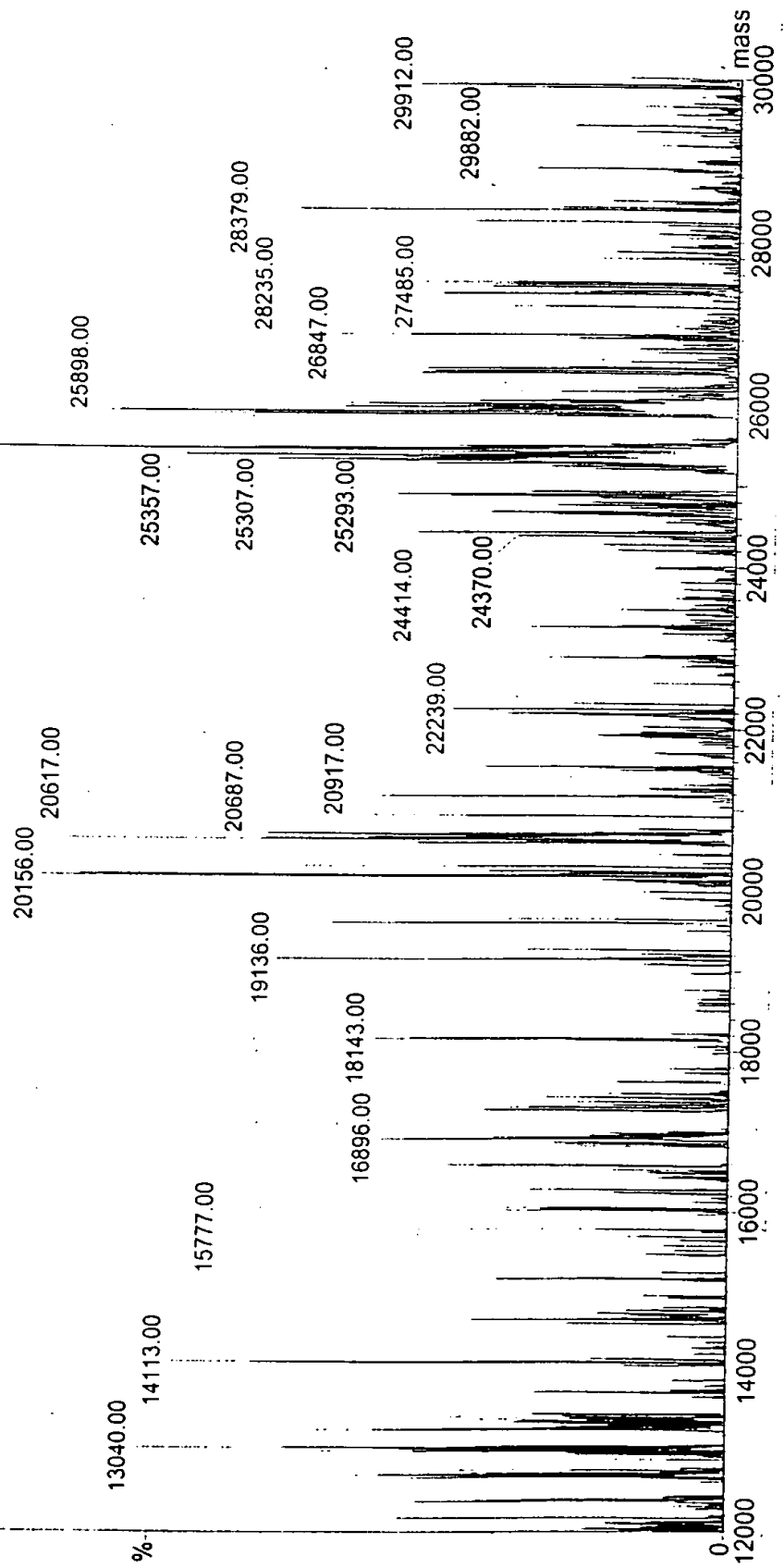


FIG. 4(d)

GOURDIN PLANT +zt

4.0

45.0

Q100-2638 20 (0.417) Mk [Ev-47894,1124] (Gs,0.750,900.1696,1.00,L33,R33); Cm (2.86)

TOF MS ES+
357
11474.32±8.77
11708.57±6.30

A:
B:

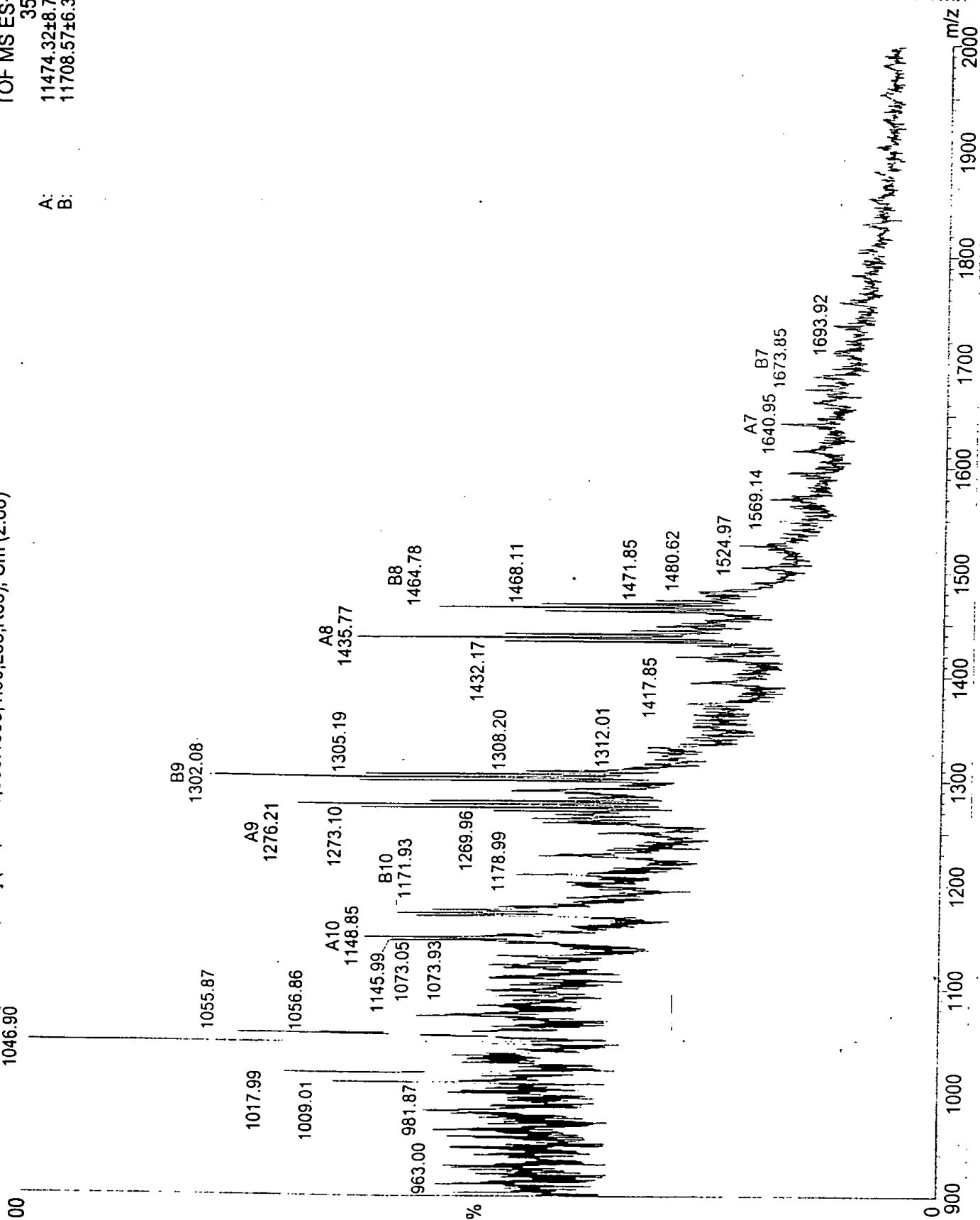
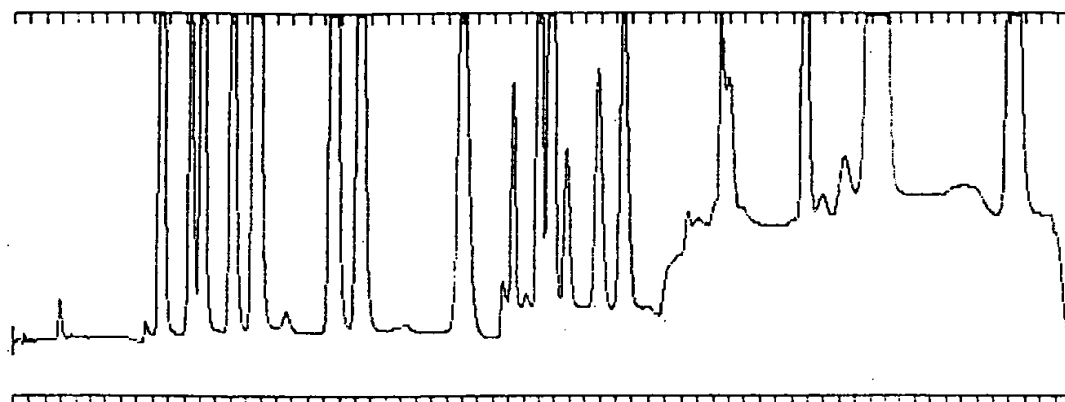


FIG. 4(e)



[Interface 0] 0-68 Min Scale: 15 Mv Ch.A, 15 Mv Ch.B
 amino acid analysis Processed: 11-22-2000 14:26:30, segment 17, cycle 936
 RAW DATA SAVED IN FILE K:AAA936.PTS Second Channel Stored in K:BAA936.PTS

***** EXTERNAL STANDARD TABLE *****
 ***** 11-22-2000 14:26:33 Version 4.1 *****
 * Sample Name: amino acid analysis Data File: K:AAA936 *
 * Date: 11-22-2000 14:26:30 Method: F:REBECKA 11-22-2000 13:54:21 # 457*
 * Interface: 0 Cycle#: 936 Operator jmc Channel#: 0 Vial#: N.A. *
 * Starting Peak Width: 21 Threshold: .5 Area Threshold: 500 *

 Starting Delay: 0.00 Ending retention time: 68.00
 Area reject: 5000 One sample per 2.002 sec.
 Amount injected: 1.00 Dilution factor: 1.00
 Sample Weight: 1.000000

PEAK NUM	RET TIME	PEAK NAME	CONCENTRATION in naoles	NORMALIZED CONC	AREA	HEIGHT	AREA/ HEIGHT	REF PEAK	% DELTA RET TIME	CONC/AREA
1	2.936	cysae	0.0711	0.1504%	20695	1550	13.4 1	6	-1.592	3.4373E-06
2	8.609	cacys	0.0410	0.0866%	9566	696	13.7 1	6	0	4.2818E-06
3	9.543	asx	3.6346	7.6853%	1019304	61489	16.6 1	6	.5811	3.5658E-06
4	11.378	thr	1.1549	2.4420%	314916	15245	20.7 2	6	.1132	3.6674E-06
5	12.112	ser	2.0456	4.3254%	595007	27668	21.5 2	6	0	3.4380E-06
6	14.081	int. std.	1.0397	2.1985%	576309	23599	24.4 2	6	0	1.8041E-06
7	15.649	glx	6.6195	13.9967%	1959672	71617	27.4 2	6	.1667	3.3779E-06
8	17.651	pro + cys	(2.1133) 2.9045	6.1414%	28161	809	34.8 2	6	-.2854	1.0314E-04
9	20.554	gly	3.4509	7.2968%	1098728	36599	30.0 2	9	0	3.1408E-06
10	22.256	ala	2.8168	5.9561%	801412	25276	31.7 2	9	0	3.5148E-06
11	28.996	val	2.616 2.5700	5.4358%	703543	16490	42.7 1	9 7.15 8.77	0	3.6541E-06
12	32.299	met	0.5625	1.1894%	157161	8772	17.9 1	16	.0101	3.5792E-06
13	33.166		0.0000	0.0000%	10132	523	19.4 1			0.0000E+00
14	33.967	ileu	1.8404	3.8914%	535119	23330	22.9 2	16	-.0931	3.4392E-06
15	34.735	leu	3.1701	6.7031%	953284	38035	25.1 2	16	0	3.3255E-06
16	35.802	nl-std.	0.2733	0.5791%	163238	6196	26.3 2	16	0	1.6777E-06
17	37.871	tyr	1.0645	2.2508%	290327	9412	30.8 1	16	0	3.6666E-06
18	39.473	phe	1.6115	3.4075%	408260	12881	31.7 1	16	0	3.9472E-06
19	45.479	his	(1.211) 1.2633	2.6711%	203562	8185	24.9 2	16	0	6.2059E-06
20	46.013		0.0000	0.0000%	154147	5442	28.3 2			0.0000E+00
21	50.751	lys	1.2451	2.6327%	385456	13267	29.1 2	16	0	3.2302E-06
22	51.885	trp	0.1950	0.3929%	32441	913	35.5 2	16	0	5.7275E-06
23	53.287		0.0000	0.0000%	102408	2246	45.6 2			0.0000E+00
24	55.355	NH4	6.1666	13.0391%	3568074	61370	57.7 2	16	0	1.7279E-06
25	64.197	arg	3.5602	7.5279%	1016938	22156	45.9 1	16	0	3.5009E-06

TOTAL AMOUNT: 47.2334

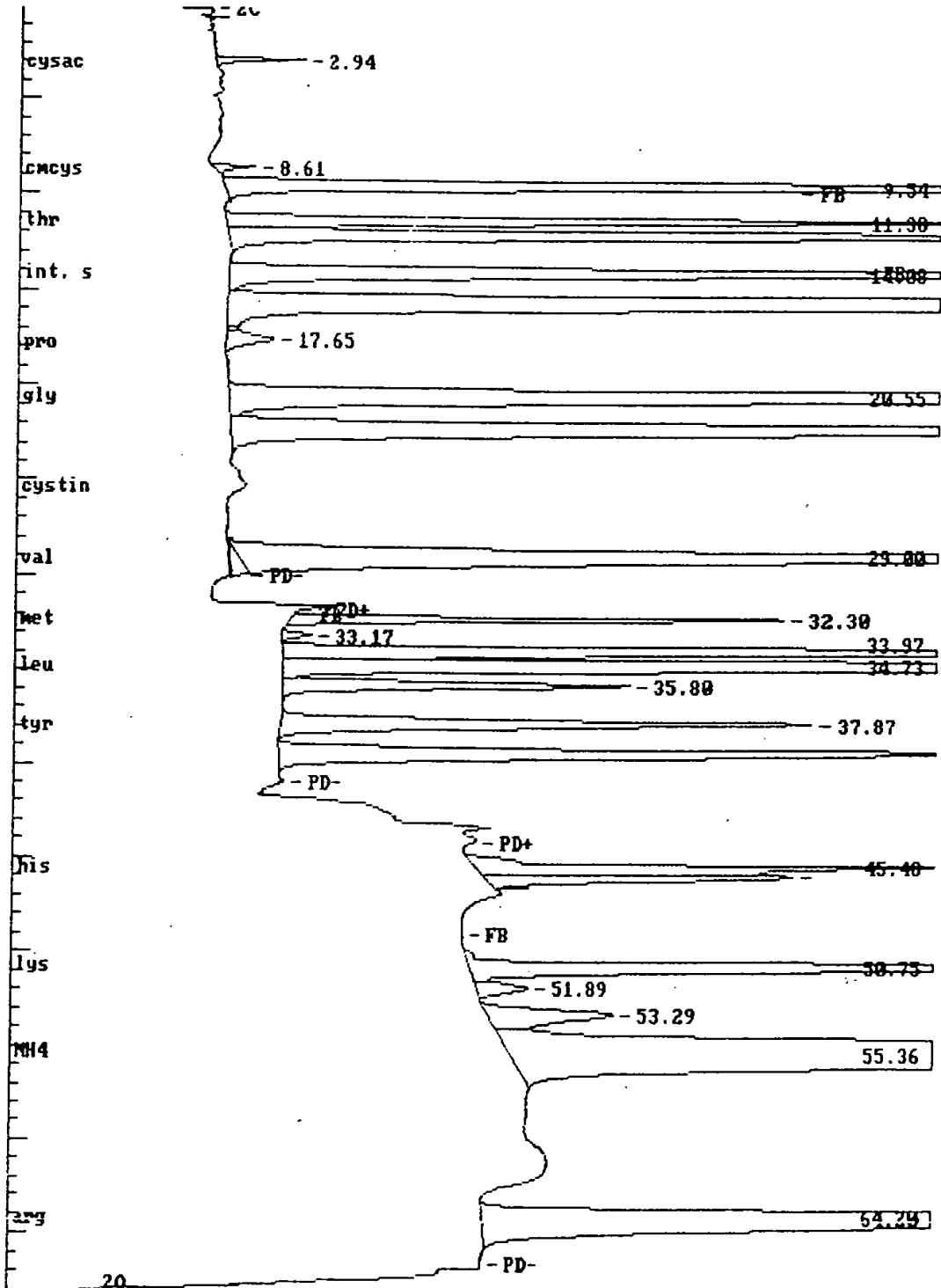
FIG. 5(a)

Areas, times, and heights stored in: K:AAA936.ATB

Data File = K:AAA936.PTS Printed on 11-22-2000 at 14:27:06

Start time: 0.00 min. Stop time: 68.00 min. Offset: 0 mv.

Full Range: 15 millivolts



EXTERNAL STANDARD TABLE

FIG.5(b)

 * Sample Name: amino acid analysis Data File: K:BAA936 *
 * Date: 11-22-2000 14:26:30 Method: F:SEBECKA 11-22-2000 13:55:21 # 257 *
 * Interface: 0 Cycle#: 936 Operator jmc Channel#: 1 Vial#: N.A. *
 * Starting Peak Width: 21 Threshold: .5 Area Threshold: 500 *

 Starting Delay: 0.00 Ending retention time: 68.00
 Area reject: 5000 One sample per 2.002 sec.
 Amount injected: 1.00 Dilution factor: 1.00
 Sample Weight: 1.000000

PEAK NUM	RET TIME	PEAK NAME	CONCENTRATION in nmoles	NORMALIZED CONC	AREA	HEIGHT	AREA/ HEIGHT	REF PEAK	% DELTA RET TIME	CONC/AREA
1	3.775		0.0000	0.0000%	5143	235	18.0 1			0.0000E+00
2	9.510		0.0000	0.0000%	129394	7707	16.8 1			0.0000E+00
3	11.345		0.0000	0.0000%	24969	1171	21.3 2			0.0000E+00
4	12.079		0.0000	0.0000%	59186	2389	24.7 2			0.0000E+00
5	14.047		0.0000	0.0000%	47121	1978	23.8 1			0.0000E+00
6	15.616	glx	6.2317	74.6757%	375516	13802	27.2 1	7	.2393	1.6595E-05
7	17.651	pro+cys	(2.1133)	25.3244%	199944	6665	30.0 1	7	0	1.0570E-05
8	20.554		0.0000	0.0000%	83682	2753	30.4 1			0.0000E+00
9	22.222		0.0000	0.0000%	67237	2027	33.2 1			0.0000E+00

TOTAL AMOUNT = 8.3451

Areas, times, and heights stored in: K:BAA936.ATB

Data File = K:BAA936.PTS Printed on 11-22-2000 at 14:28:59

Start time: 0.00 min. Stop time: 68.00 min. Offset: -95 mv.

Full Range: 15 millivolts

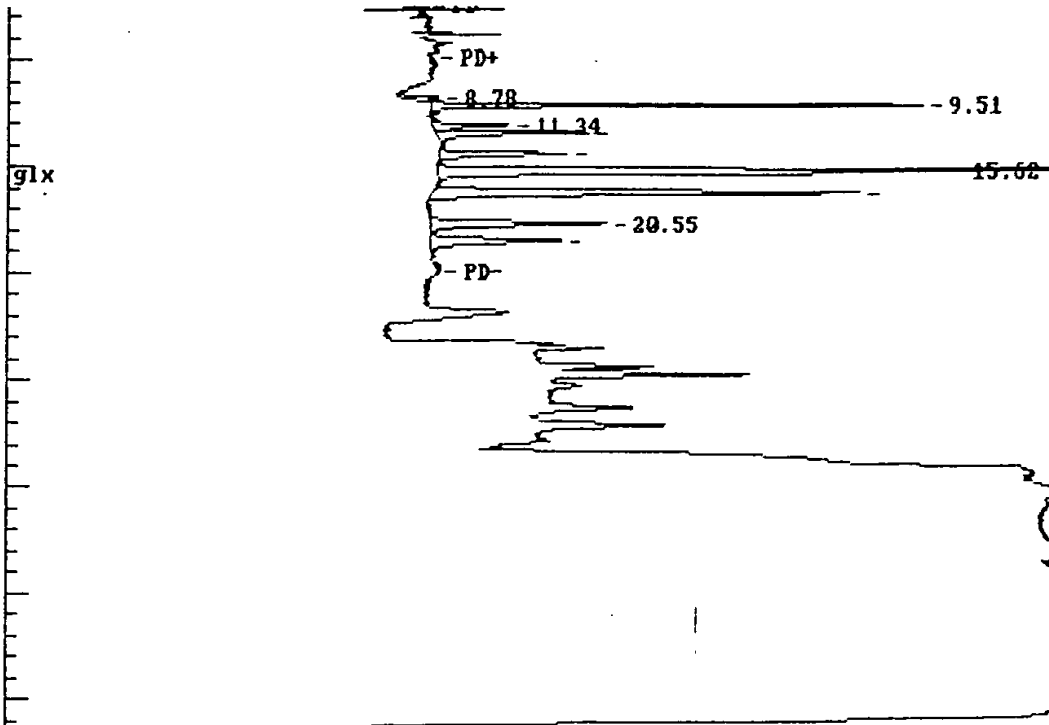


FIG.5(c)